DeClout
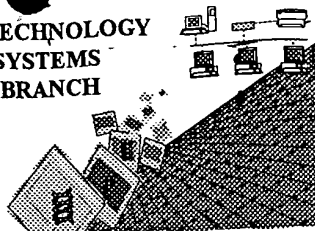
RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/857,097A_

Source: _1600 RUSH_

Date Processed by STIC: _9/19/2002_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
> **http://www.uspto.gov/web/offices/pac/checker**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**http://www.uspto.gov/ebc/efs/downloads/documents.htm**> , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. **Hand Carry directly to:**
    U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
    Or
    U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. **Federal Express, United Parcel Service, or other** delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/857,097A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics / Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ____ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ✓ Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length — Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ____ Skipped Sequences (OLD RULES) — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped. Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences (NEW RULES) — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000

9 ____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213> Response — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence.

11 ____ Use of <220> — Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n — n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

1600

```
RAW SEQUENCE LISTING              DATE: 09/19/2002
PATENT APPLICATION:  US/09/857,097A    TIME: 13:04:24

          Input Set : A:\EP.txt
          Output Set: N:\CRF4\09192002\I857097A.raw

    4 <110> APPLICANT: Urbaniak, Stanislaw J.
    5        Barker, Robert N.
    7 <120> TITLE OF INVENTION: ALLO- AND AUTO-REACTIVE T-CELL EPITOPES
    9 <130> FILE REFERENCE: P097
   11 <140> CURRENT APPLICATION NUMBER: 09/857,097A
   12 <141> CURRENT FILING DATE: 1999-12-01
   14 <150> PRIOR APPLICATION NUMBER: 9826378.3
   15 <151> PRIOR FILING DATE: 1998-12-01
E--> 17 <160> NUMBER OF SEQ ID NOS: (152) 46 (p.6)
   19 <170> SOFTWARE: PatentIn Ver. 2.1
```

Does Not Comply
Corrected Diskette Needed

pp 1-6

global error
misaligned amino
acid numbers
(see
item 3 on Error
Summary Sheet)

same error

```
ERRORED SEQUENCES

   21 <210> SEQ ID NO: 1
   22 <211> LENGTH: 15
   23 <212> TYPE: PRT
   24 <213> ORGANISM: Homo sapiens
   26 <220> FEATURE:
   27 <223> OTHER INFORMATION: RhCE (R2 cE) Residues 2-16
   29 <400> SEQUENCE: 1
   30 Ser Ser Lys Tyr Pro Arg Ser Val Arg Arg Cys Leu Pro Leu Trp
E--> 31   1   1           5   5           10           10  15
   35 <210> SEQ ID NO: 2
   36 <211> LENGTH: 15
   37 <212> TYPE: PRT
   38 <213> ORGANISM: Homo sapiens
   40 <220> FEATURE:
   41 <223> OTHER INFORMATION: RhCE (R2 cE) Residues 12-26
   43 <400> SEQUENCE: 2
   44 Cys Leu Pro Leu Trp Ala Leu Thr Leu Glu Ala Ala Leu Ile Leu
E--> 45   1               5                   10              15
   46 <210> SEQ ID NO: 3
   49 <211> LENGTH: 15
   50 <212> TYPE: PRT
   51 <213> ORGANISM: Homo sapiens
   53 <220> FEATURE:
   54 <223> OTHER INFORMATION: RhCE (R2 cE) Residue 22-36    same
   56 <400> SEQUENCE: 3
   57 Ala Ala Leu Ile Leu Leu Phe Tyr Phe Phe Thr His Tyr Asp Ala
E--> 58   1               5                   10              15
   62 <210> SEQ ID NO: 4
   63 <211> LENGTH: 15
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RAW SEQUENCE LISTING   DATE: 09/19/2002
PATENT APPLICATION: US/09/857,097A   TIME: 13:04:24

Input Set : A:\EP.txt
Output Set: N:\CRF4\09192002\I857097A.raw

```
       64 <212> TYPE: PRT
       65 <213> ORGANISM: Homo sapiens
       67 <220> FEATURE:
       68 <223> OTHER INFORMATION: RhCE (R2 cE) Residues 32-46
       70 <400> SEQUENCE: 4
       71 Thr His Tyr Asp Ala Ser Leu Glu Asp Gln Lys Gly Leu Val Ala          same
E--> 72    1                    5                    10                                     15
       76 <210> SEQ ID NO: 5
       77 <211> LENGTH: 15
       78 <212> TYPE: PRT
       79 <213> ORGANISM: Homo sapiens
       81 <220> FEATURE:
       82 <223> OTHER INFORMATION: RhCE (R2 cE) Residue 42-56          same
       84 <400> SEQUENCE: 5
       85 Lys Gly Leu Val Ala Ser Tyr Gln Val Gly Gln Asp Leu Thr Val
E--> 86    1                    5                    10                                     15
       89 <210> SEQ ID NO: 6
       90 <211> LENGTH: 15
       91 <212> TYPE: PRT
       92 <213> ORGANISM: Homo sapiens
       93 <220> FEATURE:
       94 <223> OTHER INFORMATION: RhCE (R2 cE) Residue 52-66
       97 <400> SEQUENCE: 6                                          same
       98 Gln Asp Leu Thr Val Met Ala Ala Leu Gly Leu Gly Phe Leu Thr
E--> 99    1                    5                    10                                     15
      103 <210> SEQ ID NO: 7
      104 <211> LENGTH: 15
      105 <212> TYPE: PRT
      106 <213> ORGANISM: Homo sapiens
      108 <220> FEATURE:
      109 <223> OTHER INFORMATION: RhCE (R2 cE) Residue 62-76
      111 <400> SEQUENCE: 7
      112 Leu Gly Phe Leu Thr Ser Asn Phe Arg Arg His Ser Trp Ser Ser
E--> 113   1                    5                    10          same                       15
      117 <210> SEQ ID NO: 8
      118 <211> LENGTH: 15
      119 <212> TYPE: PRT
      120 <213> ORGANISM: Homo sapiens
      122 <220> FEATURE:
      123 <223> OTHER INFORMATION: RhCE (R2 cE) Residue 72-86
      125 <400> SEQUENCE: 8
      126 His Ser Trp Ser Ser Val Ala Phe Asn Leu Phe Met Leu Ala Leu          same
E--> 127   1                    5                    10                                     15
      131 <210> SEQ ID NO: 9
      132 <211> LENGTH: 15
      133 <212> TYPE: PRT
      134 <213> ORGANISM: Homo sapiens
      136 <220> FEATURE:
      137 <223> OTHER INFORMATION: RhCE (R2 cE) Residue 82-96
```

p.3

```
       139 <400> SEQUENCE: 9
       140 Phe Met Leu Ala Leu Gly Val Gln Trp Ala Ile Leu Leu Asp Gly        same
E--> 141      1                    5                    10                                      15
       146 <210> SEQ ID NO: 10
       147 <211> LENGTH: 15
       148 <212> TYPE: PRT
       149 <213> ORGANISM: Homo sapiens
       151 <220> FEATURE:
       152 <223> OTHER INFORMATION: RhCE (R2 cE) Residue 92-106
       154 <400> SEQUENCE: 10                                                 same
       155 Ile Leu Leu Asp Gly Phe Leu Ser Gln Phe Pro Pro Gly Lys Val
E--> 156      1                    5                    10                                      15
       160 <210> SEQ ID NO: 11
       161 <211> LENGTH: 15
       162 <212> TYPE: PRT
       163 <213> ORGANISM: Homo sapiens
       165 <220> FEATURE:
       166 <223> OTHER INFORMATION: RhCE (R2 cE) Residue 102-116            same
       168 <400> SEQUENCE: 11
       169 Pro Pro Gly Lys Val Val Ile Thr Leu Phe Ser Ile Arg Leu Ala
E--> 170      1                    5                    10                                      15
       174 <210> SEQ ID NO: 12
       175 <211> LENGTH: 15
       176 <212> TYPE: PRT
       177 <213> ORGANISM: Homo sapiens
       179 <220> FEATURE:
       180 <223> OTHER INFORMATION: RhCE (R2 cE) Residue 112-126            same
       182 <400> SEQUENCE: 12
       183 Ser Ile Arg Leu Ala Thr Met Ser Ala Met Ser Val Leu Ile Ser
E--> 184      1                    5                    10                                      15
       185 <210> SEQ ID NO: 13
       186 <211> LENGTH: 15
       187 <212> TYPE: PRT
       188 <213> ORGANISM: Homo sapiens
       190 <220> FEATURE:
       193 <223> OTHER INFORMATION: RhCE (R2 cE) Residue 122-136            same
       195 <400> SEQUENCE: 13
       196 Ser Val Leu Ile Ser Ala Gly Ala Val Leu Gly Lys Val Asn Leu
E--> 197      1                    5                    10                                      15
       201 <210> SEQ ID NO: 14
       202 <211> LENGTH: 15
       203 <212> TYPE: PRT
       204 <213> ORGANISM: Homo sapiens
       206 <220> FEATURE:
       207 <223> OTHER INFORMATION: RhCE (R2 cE) Residue 132-146         same
       209 <400> SEQUENCE: 14
       210 Gly Lys Val Asn Leu Ala Gln Leu Val Val Met Val Leu Val Glu
E--> 211      1                    5                    10                                      15
       215 <210> SEQ ID NO: 15
```

p.4

```
     216 <211> LENGTH: 15
     217 <212> TYPE: PRT
     218 <213> ORGANISM: Homo sapiens
     220 <220> FEATURE:
     221 <223> OTHER INFORMATION: RhCE (R2 cE) Residue 142-156
     223 <400> SEQUENCE: 15                                        same
     224 Met Val Leu Val Glu Val Thr Ala Leu Gly Thr Leu Arg Met Val
E--> 225     1                   5                   10                              15
     229 <210> SEQ ID NO: 16
     230 <211> LENGTH: 15
     231 <212> TYPE: PRT
     232 <213> ORGANISM: Homo sapiens
     234 <220> FEATURE:
     235 <223> OTHER INFORMATION: RhCE (R2 cE) Residue 152-166
     241 <400> SEQUENCE: 16                                        same
     242 Thr Leu Arg Met Val Ile Ser Asn Ile Phe Asn Thr Asp Tyr His
E--> 243     1                   5                   10                              15
     247 <210> SEQ ID NO: 17
     248 <211> LENGTH: 15
     249 <212> TYPE: PRT
     250 <213> ORGANISM: Homo sapiens
     252 <220> FEATURE:
     253 <223> OTHER INFORMATION: RhCE (R2 cE) Residue 162-176        same
     255 <400> SEQUENCE: 17
     256 Asn Thr Asp Tyr His Met Asn Leu Arg His Phe Tyr Val Phe Ala
E--> 257     1                   5                   10                              15
     261 <210> SEQ ID NO: 18
     262 <211> LENGTH: 15
     263 <212> TYPE: PRT
     264 <213> ORGANISM: Homo sapiens
     266 <220> FEATURE:
     267 <223> OTHER INFORMATION: RhCE (R2 cE) Residue 172-186        same
     269 <400> SEQUENCE: 18
     270 Phe Tyr Val Phe Ala Ala Tyr Phe Gly Leu Thr Val Ala Trp Cys
E--> 271     1                   5                   10                              15
     275 <210> SEQ ID NO: 19
     276 <211> LENGTH: 15
     277 <212> TYPE: PRT
     278 <213> ORGANISM: Homo sapiens
     281 <220> FEATURE:
     282 <223> OTHER INFORMATION: RhCE (R2 cE) Residue 182-196        same
     284 <400> SEQUENCE: 19
     285 Thr Val Ala Trp Cys Leu Pro Lys Pro Leu Pro Lys Gly Thr Glu
E--> 286     1                   5                   10                              15
     291 <210> SEQ ID NO: 20
     292 <211> LENGTH: 15
     293 <212> TYPE: PRT
     294 <213> ORGANISM: Homo sapiens
     296 <220> FEATURE:
```

p.S

RAW SEQUENCE LISTING   DATE: 09/19/2002
PATENT APPLICATION: US/09/857,097A   TIME: 13:04:24

Input Set : A:\EP.txt
Output Set: N:\CRF4\09192002\I857097A.raw

297 <223> OTHER INFORMATION: RhCE (R2 cE) Residue 192-206   *same*
299 <400> SEQUENCE: 20
300 Pro Lys Gly Thr Glu Asp Asn Asp Gln Arg Ala Thr Ile Pro Ser
E--> 301   1   5   10   15

IMPORTANT The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

<210> 46 ← *last sequence in submitted file*
<211> 15
<212> PRT
<213> Homo sapiens

<220>
<223> RhCE (R1 Ce) Residue 222-236

where are amino acids?

Input Set : **A:\EP.txt**
Output Set: **N:\CRF4\09192002\I857097A.raw**

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 31
Seq#:4; Line(s) 72
Seq#:6; Line(s) 99
Seq#:7; Line(s) 113
Seq#:8; Line(s) 127
Seq#:9; Line(s) 141
Seq#:14; Line(s) 211
Seq#:15; Line(s) 225
Seq#:17; Line(s) 257
Seq#:18; Line(s) 271
Seq#:22; Line(s) 328
Seq#:24; Line(s) 356
Seq#:36; Line(s) 524
Seq#:39; Line(s) 565
Seq#:41; Line(s) 595
Seq#:42; Line(s) 609
Seq#:43; Line(s) 627
Seq#:44; Line(s) 641
Seq#:45; Line(s) 656

VERIFICATION SUMMARY   DATE: 09/19/2002
PATENT APPLICATION: US/09/857,097A   TIME: 13:04:25

Input Set : **A:\EP.txt**
Output Set: **N:\CRF4\09192002\I857097A.raw**

```
L:31 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:45 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:58 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:72 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4
L:86 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5
L:93 M:283 W: Missing Blank Line separator, <220> field identifier
L:99 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6
L:113 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7
L:127 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
L:141 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9
L:156 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10
L:170 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:11
L:184 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:12
L:197 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:13
L:211 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:14
L:225 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:15
L:243 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:257 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
L:271 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:18
L:286 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:19
L:301 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:20
L:315 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:21
L:328 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:22
L:342 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:23
L:356 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:24
L:369 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:25
L:380 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:26
L:395 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:27
L:408 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:28
L:422 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:29
L:438 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:30
L:452 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:31
L:467 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:32
L:483 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:33
L:497 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:34
L:511 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35
L:524 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:36
L:539 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:37
L:553 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:38
L:565 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:39
L:581 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:40
L:595 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:41
L:609 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:42
L:627 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:43
L:641 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:44
L:656 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:45
L:17 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (152) Counted (45)
```